

Ramneek Gupta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/881160/publications.pdf>

Version: 2024-02-01

83
papers

11,578
citations

117625

34
h-index

98798

67
g-index

88
all docs

88
docs citations

88
times ranked

21458
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. <i>Proteomics</i> , 2004, 4, 1633-1649.	2.2	1,784
2	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. <i>EMBO Journal</i> , 2013, 32, 1478-1488.	7.8	1,130
3	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. <i>Glycobiology</i> , 2005, 15, 153-164.	2.5	825
4	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	27.8	750
5	Analysis and prediction of leucine-rich nuclear export signals. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 527-536.	2.1	721
6	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
7	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	27.8	500
8	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. <i>Nature Genetics</i> , 2014, 46, 51-55.	21.4	497
9	Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut. <i>Nature Microbiology</i> , 2016, 1, 16093.	13.3	321
10	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	4.2	312
11	Whole grain-rich diet reduces body weight and systemic low-grade inflammation without inducing major changes of the gut microbiome: a randomised cross-over trial. <i>Gut</i> , 2019, 68, 83-93.	12.1	278
12	Prediction of glycosylation across the human proteome and the correlation to protein function. , 2001, , .		276
13	Prediction of glycosylation across the human proteome and the correlation to protein function. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 310-22.	0.7	246
14	Prediction of human protein function according to Gene Ontology categories. <i>Bioinformatics</i> , 2003, 19, 635-642.	4.1	233
15	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	27.8	230
16	Choice of bacterial DNA extraction method from fecal material influences community structure as evaluated by metagenomic analysis. <i>Microbiome</i> , 2014, 2, 19.	11.1	228
17	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013, 45, 902-906.	21.4	221
18	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. <i>Nucleic Acids Research</i> , 1999, 27, 370-372.	14.5	213

#	ARTICLE	IF	CITATIONS
19	NESbase version 1.0: a database of nuclear export signals. <i>Nucleic Acids Research</i> , 2003, 31, 393-396.	14.5	195
20	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	12.8	164
21	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	27.8	130
22	Transcriptome analysis of root-knot nematode (<i>Meloidogyne incognita</i>)-infected tomato (<i>Solanum lycopersicum</i>) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	4.2	127
23	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018, 9, 4630.	12.8	124
24	Transcriptome profiling of brown adipose tissue during cold exposure reveals extensive regulation of glucose metabolism. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 308, E380-E392.	3.5	105
25	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2017, 49, 1141-1147.	21.4	105
26	Scanning the available <i>Dictyostelium discoideum</i> proteome for O-linked GlcNAc glycosylation sites using neural networks. <i>Glycobiology</i> , 1999, 9, 1009-1022.	2.5	99
27	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. <i>Journal of Medical Genetics</i> , 2012, 49, 58-65.	3.2	96
28	Establishment and characterization of models of chemotherapy resistance in colorectal cancer: Towards a predictive signature of chemoresistance. <i>Molecular Oncology</i> , 2015, 9, 1169-1185.	4.6	91
29	Inherited coding variants at the <i>CDKN2A</i> locus influence susceptibility to acute lymphoblastic leukaemia in children. <i>Nature Communications</i> , 2015, 6, 7553.	12.8	72
30	Nationwide germline whole genome sequencing of 198 consecutive pediatric cancer patients reveals a high incidence of cancer prone syndromes. <i>PLoS Genetics</i> , 2020, 16, e1009231.	3.5	64
31	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: rationale and design of the epidemiological studies within the IMI DIRECT Consortium. <i>Diabetologia</i> , 2014, 57, 1132-1142.	6.3	48
32	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. <i>PLoS Medicine</i> , 2020, 17, e1003149.	8.4	47
33	Cerebellar mutism syndrome in children with brain tumours of the posterior fossa. <i>BMC Cancer</i> , 2017, 17, 439.	2.6	38
34	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	3.7	36
35	Acquisition of docetaxel resistance in breast cancer cells reveals upregulation of <i>ABCB1</i> expression as a key mediator of resistance accompanied by discrete upregulation of other specific genes and pathways. <i>Tumor Biology</i> , 2015, 36, 4327-4338.	1.8	36
36	Trypsin-encoding <i>PRSS1-PRSS2</i> variations influence the risk of asparaginase-associated pancreatitis in children with acute lymphoblastic leukemia: a Ponte di Legno toxicity working group report. <i>Haematologica</i> , 2019, 104, 556-563.	3.5	36

#	ARTICLE	IF	CITATIONS
37	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	3.3	34
38	Obesity is associated with depot-specific alterations in adipocyte DNA methylation and gene expression. <i>Adipocyte</i> , 2017, 6, 124-133.	2.8	34
39	Genetic predisposition to <i>PEG</i> asparaginase hypersensitivity in children treated according to <i>NOPHO ALL</i> 2008. <i>British Journal of Haematology</i> , 2019, 184, 405-417.	2.5	33
40	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , 2018, 61, 117-129.	6.3	32
41	Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 57239-57253.	1.8	30
42	Germ Cell Cancer and Multiple Relapses: Toxicity and Survival. <i>Journal of Clinical Oncology</i> , 2015, 33, 3116-3123.	1.6	29
43	Genome-wide analysis of cytogenetic aberrations in <i>ETV6</i> / <i>RUNX1</i> positive childhood acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2012, 157, 476-482.	2.5	25
44	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. <i>Diabetologia</i> , 2019, 62, 1601-1615.	6.3	22
45	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. <i>Npj Genomic Medicine</i> , 2016, 1, 16035.	3.8	21
46	Cost-effective multiplexing before capture allows screening of 25,000 clinically relevant SNPs in childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2011, 25, 1001-1006.	7.2	20
47	Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. <i>PLoS ONE</i> , 2013, 8, e68370.	2.5	20
48	Candidate single nucleotide polymorphisms and thromboembolism in acute lymphoblastic leukemia in A <i>NOPHO ALL</i> 2008 study. <i>Thrombosis Research</i> , 2019, 184, 92-98.	1.7	20
49	TIMP1 overexpression mediates resistance of MCF-7 human breast cancer cells to fulvestrant and down-regulates progesterone receptor expression. <i>Tumor Biology</i> , 2013, 34, 3839-3851.	1.8	18
50	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. <i>Diabetes</i> , 2021, 70, 2092-2106.	0.6	17
51	<i>Plasmodium falciparum</i> merozoite surface protein 1. Glycosylation and localization to low-density, detergent-resistant membranes in the parasitized erythrocyte. <i>FEBS Journal</i> , 2003, 270, 366-375.	0.2	16
52	Genome-Wide Assessment of the Association of Rare and Common Copy Number Variations to Testicular Germ Cell Cancer. <i>Frontiers in Endocrinology</i> , 2013, 4, 2.	3.5	14
53	Eukaryotic Glycosylation: Online Methods for Site Prediction on Protein Sequences. <i>Methods in Molecular Biology</i> , 2015, 1273, 127-137.	0.9	13
54	NT5C2 germline variants alter thiopurine metabolism and are associated with acquired NT5C2 relapse mutations in childhood acute lymphoblastic leukaemia. <i>Leukemia</i> , 2018, 32, 2527-2535.	7.2	13

#	ARTICLE	IF	CITATIONS
55	Prediction of Nephrotoxicity Associated With Cisplatin-Based Chemotherapy in Testicular Cancer Patients. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa032.	2.9	13
56	In silico determination of intracellular glycosylation and phosphorylation sites in human selectins: Implications for biological function. <i>Journal of Cellular Biochemistry</i> , 2007, 100, 1558-1572.	2.6	11
57	Data integration for prediction of weight loss in randomized controlled dietary trials. <i>Scientific Reports</i> , 2020, 10, 20103.	3.3	10
58	HExpoChem: a systems biology resource to explore human exposure to chemicals. <i>Bioinformatics</i> , 2013, 29, 1231-1232.	4.1	9
59	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020, 15, e0238648.	2.5	9
60	Effects of germline DHFR and FPGS variants on methotrexate metabolism and relapse of leukemia. <i>Blood</i> , 2020, 136, 1161-1168.	1.4	9
61	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , 2018, 13, e0189886.	2.5	9
62	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020, 12, 109.	8.2	8
63	Heterozygous deletion at the <i>RLN1</i> locus in a family with testicular germ cell cancer identified by integrating copy number variation data with phenome and interactome information. <i>Journal of Developmental and Physical Disabilities</i> , 2011, 34, e122-32.	3.6	7
64	Host genome variations and risk of infections during induction treatment for childhood acute lymphoblastic leukaemia. <i>European Journal of Haematology</i> , 2014, 92, 321-330.	2.2	7
65	The governance structure for data access in the DIRECT consortium: an innovative medicines initiative (IMI) project. <i>Life Sciences, Society and Policy</i> , 2018, 14, 20.	3.2	7
66	Polygenic risk score-analysis of thromboembolism in patients with acute lymphoblastic leukemia. <i>Thrombosis Research</i> , 2020, 196, 15-20.	1.7	3
67	Information theoretic perspective on genome clustering. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 1867-1889.	3.8	2
68	Protein annotation in the era of personal genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 335-341.	5.7	1
69	Characteristics of white blood cell count in acute lymphoblastic leukemia: A COST LEGEND phenotype-genotype study. <i>Pediatric Blood and Cancer</i> , 2022, 69, e29582.	1.5	1
70	Host Genomic Variants and Risk of Infections During Induction Treatment in Childhood Acute Lymphoblastic Leukemia. <i>Blood</i> , 2012, 120, 1382-1382.	1.4	0
71	Colorectal cancer cell lines made resistant to SN38 and Oxaliplatin: Roles of altered ion transporter function in resistance?. <i>FASEB Journal</i> , 2013, 27, lb452.	0.5	0
72	Germ cell cancer and multiple relapses: Toxicity and survival.. <i>Journal of Clinical Oncology</i> , 2015, 33, 4533-4533.	1.6	0

#	ARTICLE	IF	CITATIONS
73	Common Genetic Variants in Trypsin Regulating Genes Are Associated with Asparaginase-Associated Pancreatitis in Children with Acute Lymphoblastic Leukemia: A Ponte Di Legno Toxicity Working Group Study. <i>Blood</i> , 2017, 130, 885-885.	1.4	0
74	Title is missing!. , 2020, 16, e1009231.		0
75	Title is missing!. , 2020, 16, e1009231.		0
76	Title is missing!. , 2020, 16, e1009231.		0
77	Title is missing!. , 2020, 16, e1009231.		0
78	Title is missing!. , 2020, 17, e1003149.		0
79	Title is missing!. , 2020, 17, e1003149.		0
80	Title is missing!. , 2020, 17, e1003149.		0
81	Title is missing!. , 2020, 17, e1003149.		0
82	Title is missing!. , 2020, 17, e1003149.		0
83	Relating genomic variation to drug response in childhood acute lymphoblastic leukemia by multiplexed targeted sequencing. <i>Genome Biology</i> , 2010, 11, P41.	9.6	0